

1/4

1	CGGCACGAGGGCATGGGGCGGCTGGTTCTGCTGTGGGGAGCTGCCGTCTTCTGCTGGGA	60
1	M G R L V L L W G A A V F L L G	16
61	GGCTGGATGGCTTTGGGGCAAGGAGGAGCAGCAGAAGGAGTACAGATTCAATCATCTAC	120
17	G W M A L G Q G G A A E G V Q I Q I I Y	36
121	TTCAATTTAGAAACCGTGCAGGTGACATGGAATGCCAGCAAATACTCCAGGACCAACCTG	180
37	F N L E T V Q V T W N A S K Y S R T N L	56
181	ACTTTCCACTACAGATTCAACGGTGATGAGGCCTATGACCAGTGCACCAACTACCTTCTC	240
57	T F H Y R F N G D E A Y D Q C T N Y L L	76
241	CAGGAAGGTCACACTTCGGGGTGCCTCCTAGACGCAGAGCAGCGAGACGACATTCTCTAT	300
77	Q E G H T S G C L L D A E Q R D D I L Y	96
301	TTCTCCATCAGGAATGGGACGCACCCCGTTTTCACCGCAAGTCGCTGGATGGTTTATTAC	360
97	F S I R N G T H P V F T A S R W M V Y Y	116
361	CTGAAACCCAGTTCCCCGAAGCACGTGAGATTTTCGTGGCATCAGGATGCAGTGACGGTG	420
117	L K P S S P K H V R F S W H Q D A V T V	136
421	ACGTGTTCTGACCTGTCCTACGGGGATCTCCTCTATGAGGTTTCAGTACCGGAGCCCCTTC	480
137	T C S D L S Y G D L L Y E V Q Y R S P F	156
481	GACACCGAGTGGCAGTCCAAACAGGAAAATACCTGCAACGTCACCATAGAAGGCTTGGAT	540
157	D T E W Q S K Q E N T C N V T I E G L D	176
541	GCCGAGAAGTGTTACTCTTTCTGGGTCAGGGTGAAGGCTATGGAGGATGTATATGGGCCA	600
177	A E K C Y S F W V R V K A M E D V Y G P	196
601	GACACATACCCAAGCGACTGGTCAGAGGTGACATGCTGGCAGAGAGGCGAGATTCGGGAT	660
197	D T Y P S D W S E V T C W Q R G E I R D	216
661	GCCTGTGCAGAGACACCAACGCCTCCCAAACCAAGCTGTCCAAATTTATTTTAATTTCC	720
217	A C A E T P T P P K P K L S K F I L I S	236
721	AGCCTGGCCATCCTTCTGATGGTGTCTCTCCTCCTTCTGTCTTTATGGAAATTATGGAGA	780
237	S L A I L L M V S L L L L S L W K L W R	256
781	GTGAAGAAGTTTCTCATTCCCAGCGTGCCAGACCCGAAATCCATCTTCCCCGGGCTCTTT	840
257	V K K F L I P S V P D P K S I F P G L F	276
841	GAGATACACCAAGGGAACCTCCAGGAGTGGATCACAGACACCCAGAACGTGGCCACCTC	900
277	E I H Q G N F Q E W I T D T Q N V A H L	296

FIG. 1A

901	CACAAGATGGCAGGTGCAGAGCAAGAAAGTGGCCCCGAGGAGCCCCTGGTAGTCCAGTTG	960
297	H K M A G A E Q E S G P E E P L V V Q L	316
961	GCCAAGACTGAAGCCGAGTCTCCAGGATGCTGGACCCACAGACCGAGGAGAAAGAGGCC	1020
317	A K T E A E S P R M L D P Q T E E K E A	336
1021	TCTGGGGGATCCCTCCAGCTTCCCCACCAGCCCCCTCCAAGGCGGTGATGTGGTCACAATC	1080
337	S G G S L Q L P H Q P L Q G G D V V T I	356
1081	GGGGGCTTCACCTTTGTGATGAATGACCGCTCCTACGTGGCGTTGTGATGGACACACCAC	1140
357	G G F T F V M N D R S Y V A L *	372
1141	TGTCAAAGTCAACGTCAGGATCCACGTTGACATTTAAAGACAGAGGGGACTGTCCCGGGG	1200
1201	ACTCCACACCACCATGGATGGGAAGTCTCCACGCCAATGATGGTAGGACTAGGAGACTCT	1260
1261	GAAGACCCAGCCTCACC GCCTAATGCGGCCACTGCCCTGCTAACTTTCCCCACATGAGT	1320
1321	CTCTGTGTTCAAAGGCTTGATGGCAGATGGGAGCCAATTGCTCCAGGAGATTACTCCCA	1380
1381	GTTCTTTTCGTGCCTGAACGTTGTACATAAAACCCCAAGGCAGCACGTCCAAAATGCTG	1440
1441	TAAAACCATCTTCCCACTCTGTGAGTCCCCAGTTCCGTCCATGTACCTGTTCCATAGCAT	1500
1501	TGGATTCTCGGAGGATTTTTTGTCTGTTTTGAGACTCCAACCACCTCTACCCCTACAAA	1560
1561	AAAAAAAAAAAAA 1573	

FIG. 1B

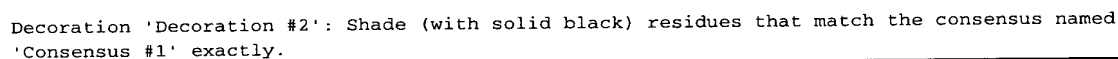
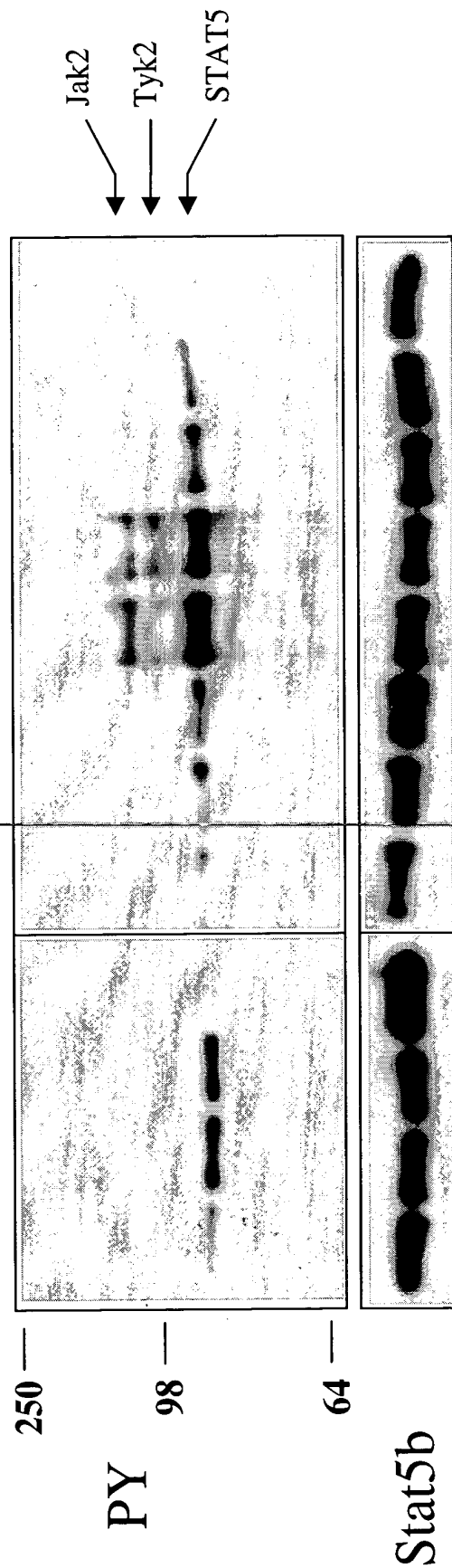
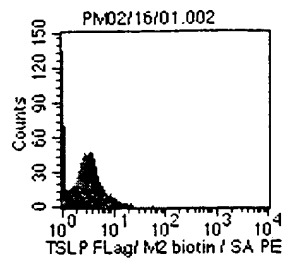
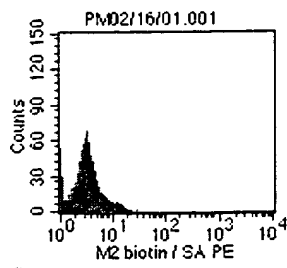
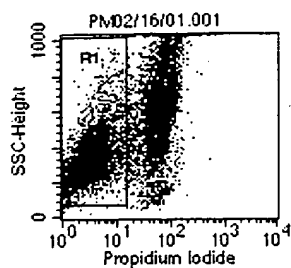


FIG. 2

Stat5b	+	+	+	+	+
IL7R α	+	+	+	+	-
IL2R β	-	-	-	-	+
Jak2	-	-	+	+	-
Jak3	+	-	-	-	-
Tyk2	-	+	+	+	+
IL2 γ c	+	-	-	-	-
CRCGCL	-	+	+	+	+
pCDNA3	+	+	-	-	+



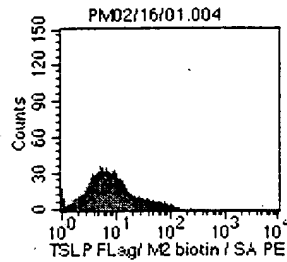
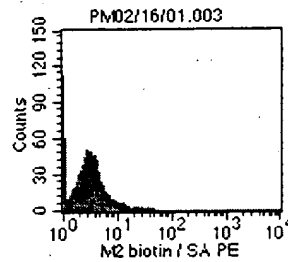
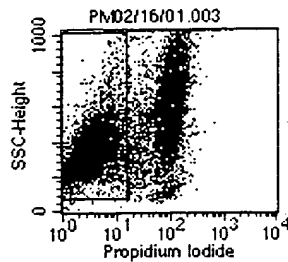
PC4



Mean
3.56

Mean
3.56

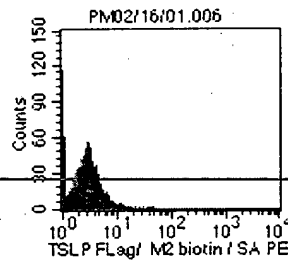
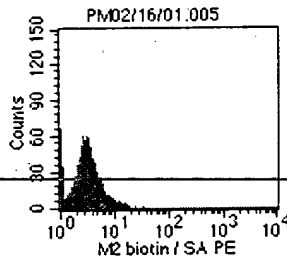
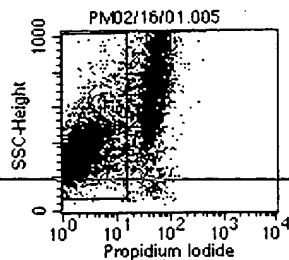
CRCGCL



Mean
3.69

Mean
11.20

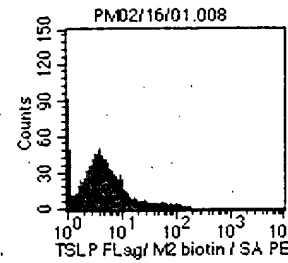
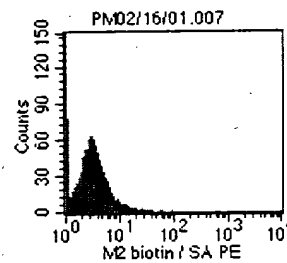
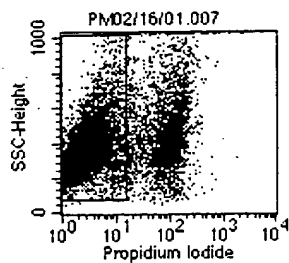
IL2 common
gamma C



Mean
3.50

Mean
3.22

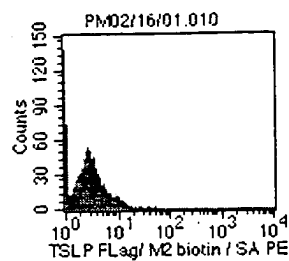
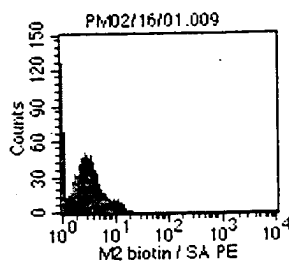
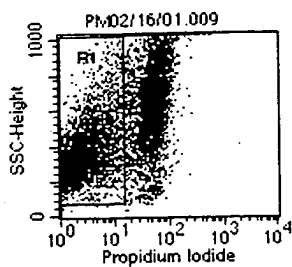
CRCGCL
+ IL7a



Mean
3.57

Mean
7.23

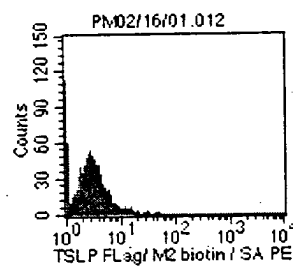
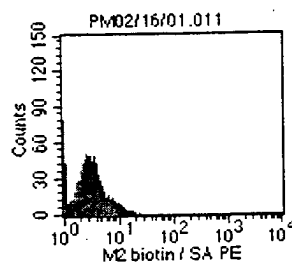
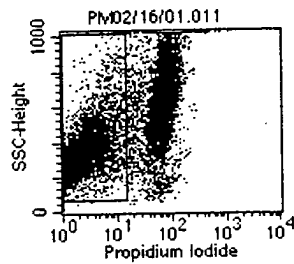
IL7a



Mean
3.46

Mean
3.41

IL2 common
gamma C + IL7a



Mean
3.60

Mean
3.41